

## REMARKS

By this amendment, Applicants have added new claims 32 and 33 directed to conducting the genotyping utilizing 12 to 40 single nucleotide polymorphisms (SNPs). Support for new claims 32 and 33 can be found in the specification, for example, at page 46, lines 7-10 and Tables 1 and 2. New claims 34 and 35 have been added and are directed to embodiments where only SNPs that are not genetically linked with respect to one another and are located outside tandem repeat nucleic acid sequences are utilized in the method. New claims 36 and 37 have been added and are directed to embodiments where methods utilizing particular SNP panels are employed in the genotyping. Support for new claims 34-37 can be found in the specification, for example, at page 4, lines 20-28 and claim 2, page 9, line 20 to page 10, line 10. These new claims do not add new matter. Applicants respectfully request entry of these amendments and allowance of the pending claims.

### Rejection Under 35 U.S.C. § 102(b)

The Examiner rejected claims 21-25 and 27-28 under 35 U.S.C. §102(b) as allegedly being anticipated by Gill (Int. J. Legal Med. Pub. 4/2001). Applicants respectfully traverse this rejection.

To establish a *prima facie* case of anticipation under 35 U.S.C. §102(b) each and every element of the claims must be disclosed in the cited prior art reference. The present claims include, among other things, that the two or more SNPs utilized in the method (i) are not genetically linked with respect to one another, and (ii) are located outside tandem repeat nucleic acid sequences.

Gill discloses using small arrays of 50-150 loci for forensic analysis. Gill requires that the loci are chosen so that alleles range in portion between 0.2 to 0.8.

### Discussion

Relatively small arrays (ca. 50 loci) are very efficient tools for human identity testing purposes, forensic stains or for distinguishing between close relatives, e.g. brothers, provided that loci are chosen so that alleles range in proportion between 0.2-0.8.

(Gill at p. 209, right column). Thus, Gill takes SNPs throughout the genome and uses

them for his analysis. Gill says nothing about selecting out two or more SNPs utilized in the claimed method that are (i) not genetically linked with respect to one another, and (ii) located outside tandem repeat nucleic acid sequences.

In fact, Gill discloses that independence (e.g., no genetic linkage) has not been assessed in this paper.

Independence assumptions have not been assessed in this paper; however, it is inevitable that due consideration will be needed with large arrays.

(Gill p. 210, left column). Thus, Gill does not realize that SNPs that are (i) not genetically linked with respect to one another, and (ii) located outside tandem repeat nucleic acid sequences can be used for, among other things, forensic identification.

With regard to new claims 32-37, Applicants can identify individuals utilizing the claimed method even when only a small number of SNPs (e.g., 12 to 40 SNPs) are available or when utilizing the claimed panels. Applicants can do this because they select SNPs that are (i) not genetically linked with respect to one another, and (ii) located outside tandem repeat nucleic acid sequences.

In contrast, Gill teaches using 50-150 loci for forensic analysis (Gill p. 204, left column) and not the small number of SNPs 12 to 40 SNPs, nor the claimed panels that can identify a compromised specimen. Accordingly, Gill does not anticipate the claims and Applicants request that the rejection under 35 U.S.C. §102 be reconsidered and withdrawn.

### **Rejections Under 35 U.S.C. §103(a)**

The Examiner rejected claims 26, and 29-31 under 35 U.S.C. §103(a) for allegedly being obvious over Gill in view of Shultz (U.S. Patent No. 6,2354,480) or Gill in view of Koster (U.S. Patent No. 6,133,436) or Gill in view of Jehaes (Int. J. Legal Med. Pub. 12/2001).

A prior art reference cannot render an invention obvious if one of ordinary skill in the art would not use the reference to solve the problem at hand or if the reference teaches away from the claimed invention. *KSR International Co. v. Teleflex Inc.* 127 S. Ct. 1727, 1734. Applicants refer the Examiner to the arguments above with regard to Gill. As discussed above, Gill does not realize that SNPs that are (i) not genetically linked with respect to one another, and (ii) located outside tandem repeat nucleic acid sequences can be used for, among other things, forensic

identification. Neither Shultz, Koster, nor Jehaes alone or in combination disclose that SNPs that are (i) not genetically linked with respect to one another, and (ii) located outside tandem repeat nucleic acid sequences can be used for, among other things, forensic identification.

Accordingly, Applicants respectfully submit the claims cannot be considered obvious over any of the cited references alone or in combination. Applicants request that the rejections under 35 U.S.C. §103(a) be reconsidered and withdrawn.

With regard to new claims 32-37, Applicants can identify individuals utilizing the claimed method even when only a small number of SNPs (e.g., 12 to 40 SNPs) are available or when utilizing the claimed panels. Gill teaches using 50-150 loci for forensic analysis (Gill p. 204, left column) and not the small number of SNPs 12 to 40 SNPs, nor the claimed panels that can identify a compromised specimen. Accordingly, Gill teaches away from using a small number of SNPs as presently claimed.

### **Conclusion**

Reconsideration and allowance are respectfully solicited.

Applicants hereby requests a three-month extension of time under 37 CFR 1.136(a) and authorize the Patent Office to charge the Deposit Account No. 11-0171.

If any additional fees are due or any overpayment has been made, please charge our Deposit Account No. 11-0171 or credit our Deposit account for such sum.

If the Examiner has any questions regarding the present application, the Examiner is cordially invited to contact Applicants' attorney at the telephone number provided below.

Respectfully submitted,

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